



1600

RAW SEQUENCE LISTING

DATE: 05/06/2003

PATENT APPLICATION: US/09/783,436A

TIME: 08:04:49

Input Set : A:\CURA172x.txt

Output Set: N:\CRF4\05062003\I783436A.raw

3 <110> APPLICANT: Vernet et al.
 5 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
 7 <130> FILE REFERENCE: 15966-672
 9 <140> CURRENT APPLICATION NUMBER: 09/783,436A
 10 <141> CURRENT FILING DATE: 2001-02-14
 12 <150> PRIOR APPLICATION NUMBER: 60/182,637
 13 <151> PRIOR FILING DATE: 2000-02-15
 15 <150> PRIOR APPLICATION NUMBER: 60/237,862
 16 <151> PRIOR FILING DATE: 2000-10-04
 18 <150> PRIOR APPLICATION NUMBER: 60/240,316
 19 <151> PRIOR FILING DATE: 2000-10-13
 21 <150> PRIOR APPLICATION NUMBER: 09/783,436
 22 <151> PRIOR FILING DATE: 2001-02-14
 24 <160> NUMBER OF SEQ ID NOS: 75
 26 <170> SOFTWARE: PatentIn Ver. 2.1
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 579
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 33 <400> SEQUENCE: 1
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 35 gagaggtttc atcctaccat gtaactctgc ttacagccta cttgcttctc accggcgtgc 120
 36 tggggacagc aaagtctgag gactctgggtt ggtgtgggcc tgtgtgcaag gagagcagtg 180
 37 gccatgggat aaggcctctg cacagctcta gaagcttcaa tcccatttcc acccatacat 240
 38 ctctttgtgc tctcacaccc ccacagccct tctggaataa gaccatcaca gcacagggtt 300
 39 tgcaagatgt ctaatgccag tcattcacag ggcagctcag accctggcct gcggtgcata 360
 40 ctaggtgact ccacatgagg tgtcatgcta gatcctgcag ggagaataag cacacacagg 420
 41 cccgtgaccc atgctgtgga cttcatgttc taggaggtag agggagacag acaagaatca 480
 42 aatgactgta ctaggccggg cgcactggct cacgcctgta atcccagcac tttggggagg 540
 43 ccgaggcagg tggatcacga ggccaggcgt tcgagacca 579
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 94
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Homo sapiens
 51 <400> SEQUENCE: 2
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 53 1 5 10 15
 55 His Val Thr Leu Leu Thr Ala Tyr Leu Leu Leu Thr Gly Val Leu Gly
 56 20 25 30
 58 Thr Ala Lys Ser Glu Asp Ser Gly Trp Cys Gly Pro Val Cys Lys Glu
 59 35 40 45
 61 Ser Ser Gly His Gly Ile Arg Pro Leu His Ser Ser Arg Ser Phe Asn
 62 50 55 60

ENTERED
p.b

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65 65 70 75 80
67 Phe Trp Asn Lys Thr Ile Thr Ala Gln Gly Leu Gln Asp Val
68 85 90
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72 <211> LENGTH: 692
73 <212> TYPE: DNA
74 <213> ORGANISM: Homo sapiens
76 <400> SEQUENCE: 3
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78 aagtacacaa atcaaggaaa cagcttcacac actgatgtta cctttaatct aacaagatct 120
79 ctataaaaca agaaaacctc tacgtacaga tcttttaaaa ttaaagcagg catctttgct 180
80 gatccacctc tataagttgc aggttgagta tctcttatct gaaatgctag agaccagaag 240
81 tgtttcaggt ttcagatatt tagattttgg aatatgtgca tatacacgag atatccaggg 300
82 gaagagaccc aagtctaaac atgaaattca tttatgtttc atatacacct catatatata 360
83 tagcctgaag gtaattttat acagtattta taatttgtcc aaggaacaaa gttttgactg 420
84 tgttttgact atgactcgtc atgtgaagtc atatgtggaa ttttccactt gtggcatcac 480
85 acaggcactc aaaaagcttc agatttgagg gcatattgga tttcgcatac tcagattagg 540
86 gatgtcaaac ccataactcag tttaccagta aaaaaacata atgtttgcaa ttactcctcc 600
87 ttttaaatat ataattatit ttggtatggg ggaaaagagt gagaacttta tttcacctgc 660
88 ccgggcagcc gctcgagccc tatagtgagt aa 692
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92 <211> LENGTH: 115
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 4
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98 1 5 10 15
100 Ile Phe Ala Tyr Thr Arg Asp Ile Gln Gly Lys Arg Pro Lys Ser Lys
101 20 25 30
103 His Glu Ile His Leu Cys Phe Ile Tyr Thr Ser Tyr Ile Tyr Ser Leu
104 35 40 45
106 Lys Val Ile Leu Tyr Ser Ile Tyr Asn Leu Ser Lys Glu Gln Ser Phe
107 50 55 60
109 Asp Cys Val Leu Thr Met Thr Arg His Val Lys Ser Tyr Val Glu Phe
110 65 70 75 80
112 Ser Thr Cys Gly Ile Thr Gln Ala Leu Lys Lys Leu Gln Ile Trp Glu
113 85 90 95
115 His Ile Gly Phe Arg Ile Phe Arg Leu Gly Met Leu Asn Pro Tyr Ser
116 100 105 110
118 Val Tyr Gln
119 115
122 <210> SEQ ID NO: 5
123 <211> LENGTH: 2351
124 <212> TYPE: DNA
125 <213> ORGANISM: Homo sapiens
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (408)

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130 <223> OTHER INFORMATION: Where n is an A, T, G, or C

132 <400> SEQUENCE: 5

133 taaaaataca aaaaatttagc cgggcgtagt ggccgggcgcc tgtagtccca gctacttggg 60

134 aggctgaggc aggagaatgg cgtgaacccg ggaggcagag cttgcagtga gccgagatcc 120

135 cgccactgca ctccagcctg ggcgacagag cgagactccg tctcaaaaaa aaaaaaaaaa 180

136 aacatcctga gccgggctg gaaaagctct ttgcagatgg cgcttccatc tctgcgcccc 240

137 tcgggggtgg ggctgtccca tgttgtcct gctggggcct ctcaggcttc ctctttgccc 300

138 acccaaaagg aaaaatccac tgcacctca cttgttgact gacgccgtgg ccagaaacat 360

W--> 139 cctggagacg ctcttccaca catggatggt gcctgctatc gatccccntg tcagctttta 420

140 tcatgccgac cagctcaagc cccaggtctc ctggatcccc aacaagcact actccggcct 480

141 ctatgggcta atgaagctgg tgcgtcccaa tgccttgccct gctgagctgg cccgcgtcat 540

142 tgtcctggac acggatgtca ccttcgcctc tgacatctcg gagctctggg cctcttttgc 600

143 tcaactttct gacacgcagg cgatcggtct tgtggagaac cagagtgaact ggtacctggg 660

144 caacctctgg aagaaccaca ggccctggcc tgccttgggc cggggattta acacaggtgt 720

145 gatcctgctg cggctggacc ggctccggca ggctggctgg gagcagatgt ggaggctgac 780

146 agccaggcgg gagctcctta gcctgcctgc cacctcactg gctgaccagg acatcttcaa 840

147 cgctgtgatc aaggagcacc cggggctagt gcagcgtctg ccttgtgtct ggaatgtgca 900

148 gctgtcagat cacacactgg ccgagcgctg ctactctgag gcgtctgacc tcaaggatgat 960

149 ccactggaac tcaccaaaga agcttcgggt gaagaacaag catgtggaat tcttccgcaa 1020

150 tttctacctg accttcctgg agtacgatgg gaacctgctg cggagagagc tctttgtgtg 1080

151 ccccagccag ccccccactg gtgctgagca gttgcagcag gccctggcac aactggacga 1140

152 ggaagacccc tgctttgagt tccggcagca gcagctcact gtgcaccgtg tgcattgtac 1200

153 tttcctgccc catgaaccgc ccccccccg gcctcacgat gtcacccttg tggccagct 1260

154 gtccatggac cggctgcaga tgttgaagc cctgtgcagg cactggcctg gcccattgag 1320

155 cctggccttg tacctgacag acgcagaagc tcagcagttc ctgcatttcg tcgaggcctc 1380

156 accagtgtct gctgcccggc aggacgtggc ctaccatgtg gtgtaccgtg aggggcccct 1440

157 ataccccgtc aaccagcttc gcaacgtggc cttggcccag gccctcacgc cttacgtctt 1500

158 cctcagtgaac attgacttcc tgctgccta ttctctctac gactacctca gggcctccat 1560

159 tgagcagctg gggctgggca gccggcgcaa ggcagcactg gtggtgccgg catttgagac 1620

160 cctgcgctac cgcttcagct tccccattc caagggtggag ctggtggcct tgctggatgc 1680

161 gggcactctc tacaccttca ggtaccacga gtggccccga ggccacgcac ccacagacta 1740

162 tgcccgctgg cgggaggctc agggcccgta ccgtgtgcaa tgggcggcca actatgaacc 1800

163 ctacgtggtg gtgccacgag actgtccccg ctatgatcct cgctttgtgg gcttcggctg 1860

164 gaacaaagtg gccacattg tggagctgga tgcccaggaa tatgagctcc tgggtgctgcc 1920

165 cgaggccttc accatccatc tgccccacgc tccaagcctg gacatctccc gcttccgctc 1980

166 cagccccacc tatcgtgact gcctccaggc cctcaaggac gaattccacc aggacttgtc 2040

167 ccgccaccat ggggtgctg ccctcaaata cctcccagcc ctgcagcagc cccagagccc 2100

168 tgcccgaggc tgaggctggg ccggcgctgc ccctcatctt agcattgggc agacaccagg 2160

169 gcaacctgac ctccgccatc cctgctatct aaattattta aggtctctgg gaagggtgg 2220

170 ggcagagcat ctgtgggggtg gggctctccc cttgctgcta ttgtatggct ggggactggt 2280

171 ctctctctgc cccagccagt ttggggctgg ttcccccatc ttgaattggt tatccctttt 2340

172 tcataattaa a 2351

175 <210> SEQ ID NO: 6

176 <211> LENGTH: 617

177 <212> TYPE: PRT

178 <213> ORGANISM: Homo sapiens

180 <220> FEATURE:

181 <221> NAME/KEY: VARIANT

182 <222> LOCATION: (50)

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Input Set : A:\CURA172x.txt

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183 <223> OTHER INFORMATION: Wherein Xaa is any amino acid as disclosed in the
 184 specification
 186 <400> SEQUENCE: 6
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 190 Arg Lys Asn Pro Leu His Leu His Leu Val Thr Asp Ala Val Ala Arg
 191 20 25 30
 193 Asn Ile Leu Glu Thr Leu Phe His Thr Trp Met Val Pro Ala Ile Asp
 194 35 40 45
 W--> 196 Pro Xaa Val Ser Phe Tyr His Ala Asp Gln Leu Lys Pro Gln Val Ser
 197 50 55 60
 199 Trp Ile Pro Asn Lys His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu
 200 65 70 75 80
 202 Val Leu Pro Asn Ala Leu Pro Ala Glu Leu Ala Arg Val Ile Val Leu
 203 85 90 95
 205 Asp Thr Asp Val Thr Phe Ala Ser Asp Ile Ser Glu Leu Trp Ala Leu
 206 100 105 110
 208 Phe Ala His Phe Ser Asp Thr Gln Ala Ile Gly Leu Val Glu Asn Gln
 209 115 120 125
 211 Ser Asp Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro
 212 130 135 140
 214 Ala Leu Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp
 215 145 150 155 160
 217 Arg Leu Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg
 218 165 170 175
 220 Arg Glu Leu Leu Ser Leu Pro Ala Thr Ser Leu Ala Asp Gln Asp Ile
 221 180 185 190
 223 Phe Asn Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro
 224 195 200 205
 226 Cys Val Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys
 227 210 215 220
 229 Tyr Ser Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys
 230 225 230 235 240
 232 Lys Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr
 233 245 250 255
 235 Leu Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe
 236 260 265 270
 238 Val Cys Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala
 239 275 280 285
 241 Leu Ala Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln
 242 290 295 300
 244 Gln Leu Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro
 245 305 310 315 320
 247 Pro Pro Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met
 248 325 330 335
 250 Asp Arg Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro
 251 340 345 350
 253 Met Ser Leu Ala Leu Tyr Leu Thr Asp Ala Glu Ala Gln Gln Phe Leu
 254 355 360 365

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DATE: 05/06/2003

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TIME: 08:04:49

Input Set : A:\CURA172x.txt

Output Set: N:\CRF4\05062003\I783436A.raw

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256 His Phe Val Glu Ala Ser Pro Val Leu Ala Ala Arg Gln Asp Val Ala
257      370      375      380
259 Tyr His Val Val Tyr Arg Glu Gly Pro Leu Tyr Pro Val Asn Gln Leu
260 385      390      395      400
262 Arg Asn Val Ala Leu Ala Gln Ala Leu Thr Pro Tyr Val Phe Leu Ser
263      405      410      415
265 Asp Ile Asp Phe Leu Pro Ala Tyr Ser Leu Tyr Asp Tyr Leu Arg Ala
266      420      425      430
268 Ser Ile Glu Gln Leu Gly Leu Gly Ser Arg Arg Lys Ala Ala Leu Val
269      435      440      445
271 Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg Phe Ser Phe Pro His Ser
272      450      455      460
274 Lys Val Glu Leu Leu Ala Leu Leu Asp Ala Gly Thr Leu Tyr Thr Phe
275 465      470      475      480
277 Arg Tyr His Glu Trp Pro Arg Gly His Ala Pro Thr Asp Tyr Ala Arg
278      485      490      495
280 Trp Arg Glu Ala Gln Ala Pro Tyr Arg Val Gln Trp Ala Ala Asn Tyr
281      500      505      510
283 Glu Pro Tyr Val Val Val Pro Arg Asp Cys Pro Arg Tyr Asp Pro Arg
284      515      520      525
286 Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Val Glu Leu Asp
287      530      535      540
289 Ala Gln Glu Tyr Glu Leu Leu Val Leu Pro Glu Ala Phe Thr Ile His
290 545      550      555      560
292 Leu Pro His Ala Pro Ser Leu Asp Ile Ser Arg Phe Arg Ser Ser Pro
293      565      570      575
295 Thr Tyr Arg Asp Cys Leu Gln Ala Leu Lys Asp Glu Phe His Gln Asp
296      580      585      590
298 Leu Ser Arg His His Gly Ala Ala Ala Leu Lys Tyr Leu Pro Ala Leu
299      595      600      605
301 Gln Gln Pro Gln Ser Pro Ala Arg Gly
302      610      615

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305 <210> SEQ ID NO: 7

306 <211> LENGTH: 812

307 <212> TYPE: DNA

308 <213> ORGANISM: Homo sapiens

310 <400> SEQUENCE: 7

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312 cacacagata atcccagcta ctcaggagga tgaggcagga gaatcgcttt aaaatgggag 120
313 gcggaggctg tagtgagcca agattgtgcc actgcactcc agcctgggca acaaagttag 180
314 actcttatct tacaagaaaa aaaagaatgc ttaggaatca actcccctcc taatgccag 240
315 acaggtgaaa tgacttgctc aggccacagt tctgcccaag ccagcaccag ccagtggcac 300
316 agcagaatgc aaggaggag tggtacctac tttcacagca taggtgctgc cggggctctc 360
317 agagcagggtg gcacagtaat aaatggcatc ccccgagtca cagcagggct tgttacaagt 420
318 cagcttgaag agcgaccagt tattctcatt gaagtggagc tcctttttct ggccgcccac 480
319 gaagagggtcc tcacatttgg ctacaaggcg ggccagggac tgggtgtaga gtccccccag 540
320 cttggcatag gtgccctcct tgctgctgat gttgctcagg agaccgtgca gctgaagctg 600
321 ggtgctcccgtggtgaggctt gactggacac gctcagctgg gaggatgagg cggagggggc 660
322 ccctttgcac tggaggccag ggctcccgc gccgcctctg ttgcccgcca gccctgctgc 720

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/06/2003
PATENT APPLICATION: US/09/783,436A TIME: 08:04:50

Input Set : A:\CURA172x.txt
Output Set: N:\CRF4\05062003\I783436A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 408
Seq#:6; Xaa Pos. 50
Seq#:75; Xaa Pos. 50